

COLLECTION OF SUNFLOWER MARKER GENES AVAILABLE FOR GENETIC STUDIES

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Genetic studies of marker characters are one of the tasks included in the co-operative programme of the subnetwork on sunflower applied genetics.

The first objective of this study is to build up a collection of marker characters in sunflower at the Research Institute for Crop Production of Prague-Ruzyně. Further on, the inheritance of different morphological characters and linkage of genes conditioning them will be determined. In the final stage a linkage map of sunflower will be established.

Perfect knowledge of morphological characters in sunflower and their inheritance is a prerequisite of the aim accomplishment mentioned above.

The present review of the inheritance of marker characters is based on the analyses of

crosses between lines with different phenotypic expressions of a larger number of characters. In addition to our experimental results, data by other authors regarding the inheritance of some characters were compared.

The analysis is based on the crosses of two or more phenotypic expressions of uniform lines in a certain character. The generations P, F₁, F₂ and B₁ were tested. As test criterion, the chi-square method in various modifications was used, and for the determination of theoretical segregation ratios our own systematics of gene interactions was applied.

The results of the inheritance studies are summarized in Table 1 which contains the following data:

1. description of the character;
2. number of genes involved;

Table 1

1	2	3	4	5	6
Scarred stem	2	rec.	13 : 2 : 1	sc	
Corky spots on the stem	1	rec.	3 : 1	so	
Glossy brown tinge of the leaf surface	1	rec.	3 : 1 36 : 18 : 10	bt	
Anthocyanin colour of leaf petioles	3	dom.	57 : 7	Pc	
Deep spots in the leaf sheaths	3	rec.	58 : 6	sh	
Slitted petioles	3	rec.	3 : 1	sl	
Green colour of leaves (deep green, ashy green)	4	rec.	13 : 3.13 : 3	cg	
Chlorotic leaf colour	1	rec.	12 : 2.75	cch	
Mutational lack of chlorophyll	1—3 all.	rec.	3 : 1.3 : 1	chl	
Mutational absence of chlorophyll	1—3 all.	rec.	3 : 1.3 : 1	cha	
Spotted leaves of variegata type (yellow and brown)	4	rec.	13 : 3.55 : 9	st	
Crenation of leaves	4	rec.	50 : 14	cr	
Spoon-like leaf	1	rec.	3 : 1	sp	
Curled leaf blade	1	rec.	3 : 1	cu	
Strengthened leaf nerves	1	rec.	3 : 1	vs	
Dense leaf nervure	2	rec.	15 : 1	vd	
Shortened leaf petioles	2	rec.	9 : 7	ps	
Multiple leaf whirls	5	rec.	3 : 1.12 : 3 : 1 1 : 2 : 1, 12 : 3 : 1.3 : 1	wm	

1	2	3	4	5	6
Yellow colour of the plant top	1	rec.	3 : 1	y	Br ₃ , 12%
Yellow tints of ligulate flowers	1—3 all.	dom.	3 : 1.3 : 1.3 : 1	L	T, 10%
Anthocyanin colour of styles	3	dom.	27 : 27 : 10	Sa	
Anthocyanin colour of the stem leaves and hypocotyle	3	dom.	45 : 3 : 16	T, Ha	
Anthocyanin colour of achenes	1	dom.	3 : 1	Tf	Ms ₁ , 1%
Red colour of flowers	3	dom.	27 : 21 : 16	Fa	
Short tubulate flowers	1	rec.	3 : 1	fl	Ms ₂ , 20%
Long tubulate flowers	2	rec.	13 : 3	ft	
Absence of ligulate flowers	3	rec.	42 : 22	fd	
Full-blossom	2	dom.	3 : 6 : 7	Bf	
White pollen colour	1	rec.	3 : 1	pa	
Coloured anthers	3	rec.	60 : 3 : 1	ag	
Phytomelanine layer in the pericarp	1	dom.	3 : 1	P	
Striped achene	1	dom.	3 : 1	S	
Deep colour of achene hypodermis	1	rec.	3 : 1	hc	
Fasciation of the stem	1	rec.	3 : 1	f	
Fascial multi-heading	3	rec.	63 : 1	mhf	
Palmette multi-heading	3	rec.	63 : 1	mhp	
Dichotomic multi-heading	3	rec.	57 : 7	mhd	
Ramification in the upper part of the plant	1	dom.	3 : 1	Br	
Wild type of branching	2	dom.	15 : 1	Br	
Wild type of branching with one main head	2	rec.	15 : 1	b	

3. dominance — recessiveness in F₁;
4. phenotypic segregation ratio in F₂;
5. gene designation;
6. linkage of genes, strength of linkage.

This review indicates that among 40 characters under investigation the monogenic inheritance was revealed only in 15 cases, while in most characters the phenotypic expression was determined by interactions between 2—5 genes. Linkage was found between four gene pairs and in three genes a larger number of alleles occurred at one locus. In the gene designation the priority of the authors that described earlier the character was respected.

The collection of markers in the Research Institute for Crop Production of Prague-Ruzyně contains several other markers in addition to the characters presented in this review. Inheritance of them is being studied. At the same time it is necessary to comment that we do not consider the data on the inheritance of sunflower characters included in the present review as definite and we continue to improve their precision. We hope that in the future the co-operation within the subnetwork on sunflower applied genetics will help increase the knowledge on inheritance of markers in sunflower to a more substantial extent than up to this time.

COLLECTION DE GÈNES MARKER DISPONIBLES POUR LES ÉTUDES DE GÉNÉTIQUE CHEZ LE TOURNESOL

Dans cet article on présente quelques données sur l'hérédité de 40 caractères marker chez le tournesol, qui représentent des caractères morphologiques de la tige, la feuille, la fleur, l'akène, et la ramification. L'hérédité monogénique a été établie pour 15 caractères, tandis que pour les autres 25 caractères on a mis en évidence un déterminisme beaucoup plus compliqué, basé sur 2—5 gènes ou allèles. Le phénomène de linkage a été déterminé dans le cas de quatre paires de gènes.

La revue de ces caractères constitue une information de base pour l'action d'organiser une collection de caractères marker et pour l'étude plus détaillée de leur contrôle génétique, qui constitue l'un des objectifs de coopération du sous-réseau de génétique appliquée du tournesol.

COLECCIÓN DE GENES MARKER PARA ESTUDIOS GENÉTICOS AL GIRASOL

En el artículo están presentados datos sobre la herencia de 40 markers al girasol, los cuales representan caracteres morfológicos del tallo, de la hoja, flor, semilla y ramificación.

La herencia monogénica fue establecida en el caso de 15 caracteres, mientras que en el caso de los demás 25 caracteres se ha puesto de relieve un determinismo mucho más complicado, basado en 2—5 genes o alelas.

El fenómeno de linkage fue determinado en el caso de cuatro pares de genes. El paso de revista de estos caracteres constituye una información básica para la acción de constituir una colección de markers y para estudiar con más detalles su control genético, el cual constituye uno de los objetivos de cooperación de la subred de genética aplicada al girasol.